



Blast 2 Sequences results

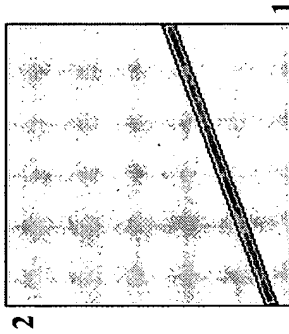
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align:

Sequence 1 lc|seq_1 Length 2112 (1 .. 2112)

Sequence 2 lc|seq_2 Length 5859 (1 .. 5859)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 4061 bits (2112), Expect = 0.0
Identities = 2112/2112 (100%)
Strand = Plus / Plus



Query: 1 ggcaatgggtcgaaattcatagaaatttgtgtgaggtgcgtagcggctctgtacaggggtg 60
|||||
Sbjct: 402 ggcaatgggtcgaaattcatagaaatttgtgtgaggtgcgtagcggctctgtacaggggtg 461

Query: 61 ctgctggagagatctctgtgtctcaggtagggcgacaaatggagaggtgttagttgccccctg 120

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|||||
Sbjct: 462 ctgcgcggagatctctggtctcaggtaggcgacaaatggagaggttagttgccccctg 521

Query: 121 tatcgctctctgcgtggcgcattgggtcatcctgccccggacatatgatatattccgctagag 180
|||||
Sbjct: 522 tatcgctctctgcgtggcgcattgggtcatcctgccccggacatatgatatattccgctagag 581

Query: 181 gattactgatagtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 240
|||||
Sbjct: 582 gattactgatagtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 641

Query: 241 gggcctgtccctcttgtcccgccctgtcctcactttttcacaaatcaaaaaaatgggcgaagc 300
|||||
Sbjct: 642 gggcctgtccctcttgtcccgccctgtcctcactttttcacaaatcaaaaaaatgggcgaagc 701

Query: 301 ccttctgttcttatagttctttagttcatcacgaaaaattacacataattatcaatagctt 360
|||||
Sbjct: 702 ccttctgttcttatagttctttagttcatcacgaaaaattacacataattatcaatagctt 761

Query: 361 attcgcttaaaaggaggagtaattgggcgcgcaaaaggaggagtaattggccgcaaaaggaggt 420
|||||
Sbjct: 762 attcgcttaaaaggaggagtaattgggcgcgcaaaaggaggagtaattggccgcaaaaggaggt 821

Query: 421 aattggccgcgcaaaaggaggagtaattgggcgcgatatcgggtgtttacatggggaggaatcc 480
|||||
Sbjct: 822 aattggccgcgcaaaaggaggagtaattgggcgcgatatcgggtgtttacatggggaggaatcc 881

Query: 481 ccttaatcatcttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 540
|||||
Sbjct: 882 ccttaatcatcttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 941

Query: 541 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatgcgcaatccgccc 600
|||||
Sbjct: 942 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatgcgcaatccgccc 1001
```

Query: 601 cgcctcagggcgctcaagctcatgcatttaatatgataccactgcgggcggccgcatggct 660
|||||
Sbjct: 1002 cgcctcagggcgctcaagctcatgcatttaatatgataccactgcgggcggccgcatggct 1061

Query: 661 gatgatgtgcgccatgaaatcggtggtgcccgcacattcgcgcaatcgacggcatgaaaaac 720
|||||
Sbjct: 1062 gatgatgtgcgccatgaaatcggtggtgcccgcacattcgcgcaatcgacggcatgaaaaac 1121

Query: 721 catgacgtgagagcctgacccccgtgttcgagggagtagccgctgcggtgttgacccat 780
|||||
Sbjct: 1122 catgacgtgagagcctgacccccgtgttcgagggagtagccgctgcggtgttgacccat 1181

Query: 781 gatgacctgcaaaagatgatcgtgacagtcggcggttggtcgatgagcgcggaatagac 840
|||||
Sbjct: 1182 gatgacctgcaaaagatgatcgtgacagtcggcggttggtcgatgagcgcggaatagac 1241

Query: 841 taccgccaggaggcaagcgcggaactcctctagtacgtggacctccgggagtacattccgt 900
|||||
Sbjct: 1242 taccgccaggaggcaagcgcggaactcctctagtacgtggacctccgggagtacattccgt 1301

Query: 901 cgtatggcggcgagtcgaaccactgggccattctcgaccgtcaaacgggtattccatctc 960
|||||
Sbjct: 1302 cgtatggcggcgagtcgaaccactgggccattctcgaccgtcaaacgggtattccatctc 1361

Query: 961 ggtagtaagtattccgtgctgctgttccagcacgtctctagtctcgccaatcttgatcgg 1020
|||||
Sbjct: 1362 ggtagtaagtattccgtgctgctgttccagcacgtctctagtctcgccaatcttgatcgg 1421

Query: 1021 atgagcgcgaaaaacctttacggtcccgaggtgcgggcgctccttgagtgccccgagggga 1080
|||||
Sbjct: 1422 atgagcgcgaaaaacctttacggtcccgaggtgcgggcgctccttgagtgccccgagggga 1481

Query: 1081 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1140
|||||
Sbjct: 1482 aagatggttcggttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1541

Query: 1141 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 1200
|||||
Sbjct: 1542 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 1601
|||||

Query: 1201 agtgtactataggctgggaagtgaagacgaccccaaccgtcgccaggcgagctggcg 1260
|||||
Sbjct: 1602 agtgtactataggctgggaagtgaagacgaccccaaccgtcgccaggcgagctggcg 1661
|||||

Query: 1261 ggttccaaggctcggtcgagatgctcgtcgagaggggcagcggaacacgatatagccccctcc 1320
|||||
Sbjct: 1662 ggttccaaggctcggtcgagatgctcgtcgagaggggcagcggaacacgatatagccccctcc 1721
|||||

Query: 1321 ttcccagaagcgggcgggatcacctacagtccacgttggtggagctgaaacgctctgct 1380
|||||
Sbjct: 1722 ttcccagaagcgggcgggatcacctacagtccacgttggtggagctgaaacgctctgct 1781
|||||

Query: 1381 ggcagcaacaaggacaaacgatctgatcgctcagacttccggcgtttctgtcgggagaga 1440
|||||
Sbjct: 1782 ggcagcaacaaggacaaacgatctgatcgctcagacttccggcgtttctgtcgggagaga 1841
|||||

Query: 1441 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagattttcgcgcaaaagta 1500
|||||
Sbjct: 1842 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagattttcgcgcaaaagta 1901
|||||

Query: 1501 gggaaagtttgagttttgaggtatttcacgcgcaaataggttaaatgactttcgtgaaaacg 1560
|||||
Sbjct: 1902 gggaaagtttgagttttgaggtatttcacgcgcaaataggttaaatgactttcgtgaaaacg 1961
|||||

Query: 1561 atgtgcaatatagcggtaagactatgaaatacacaggctggacaggctgcaaaaagcaaacgg 1620
|||||
Sbjct: 1962 atgtgcaatatagcggtaagactatgaaatacacaggctggacaggctgcaaaaagcaaacgg 2021
|||||

Query: 1621 gtgtggcgaccgcaaccatcactcgggcgtataaaaaagcggtaaaaatttcgggtataaaaaag 1680
|||||
Sbjct: 2022 gtgtggcgaccgcaaccatcactcgggcgtataaaaaagcggtaaaaatttcgggtataaaaaag 2081
|||||

Query: 1681 atgaatctggggcatgggttatagatcctgcagaattgcacagagtgttctccatccattt 1740
|||||
Sbjct: 2082 atgaatctggggcatgggttatagatcctgcagaattgcacagagtgttctccatccattt 2141

Query: 1741 caaagaaatacacccgaaacacacctaaacgcgcaagtatatgtgaagcgtgatgaaacacatg 1800
|||||
Sbjct: 2142 caaagaaatacacccgaaacacacctaaacgcgcaagtatatgtgaagcgtgatgaaacacatg 2201

Query: 1801 aaatgacctcagaaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat 1860
|||||
Sbjct: 2202 aaatgacctcagaaaatcagcgcattagagcgtgaagttcggactttacgcgatgctttat 2261

Query: 1861 ctgatgccaggaggatcgcgacaaaatggcgcgacatggccgagcgtctttcaatttcat 1920
|||||
Sbjct: 2262 ctgatgccaggaggatcgcgacaaaatggcgcgacatggccgagcgtctttcaatttcat 2321

Query: 1921 caccgatgagagaggaagaccgccccctcaaaaaacaaagatggtggaagatatctgat 1980
|||||
Sbjct: 2322 caccgatgagagaggaagaccgccccctcaaaaaacaaagatggtggaagatatctgat 2381

Query: 1981 cctgggttcaggagccttgccctttactggcggaacacgcgatatattgaggcacaggccc 2040
|||||
Sbjct: 2382 cctgggttcaggagccttgccctttactggcggaacacgcgatatattgaggcacaggccc 2441

Query: 2041 gcactttagaggcggaagcctataaacgagtaccacacactagaagccagattgaggaaa 2100
|||||
Sbjct: 2442 gcactttagaggcggaagcctataaacgagtaccacacacactagaagccagattgaggaaa 2501

Query: 2101 atagggaaactg 2112
|||||
Sbjct: 2502 atagggaaactg 2513

CPU time: 0.02 user secs. 0.02 sys. secs 0.04 total secs.

Lambda K H

Blast Result

1.33 0.621 1.12

Gapped

Lambda

K H

1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1

Number of Hits to DB: 704

Number of extensions: 18

Number of successful extensions: 13

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 2112

Length of database: 12,527,565,053

Length adjustment: 27

Effective length of query: 2085

Effective length of database: 12,527,565,026

Effective search space: 26119973079210

Effective search space used: 26119973079210

Neighboring words threshold: 0

Window for multiple hits: 0

X1: 11 (21.1 bits)

X2: 26 (50.0 bits)

X3: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 22 (43.0 bits)